GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 18, 2002, 10:41:48 ; Search time 21 Seconds
(without alignments)
2681.350 Million cell updates/sec

Title: US-09-802-668-105
Perfect score: 3114
Sequence: 1 GTGPEFPGSRPALGPLSYRE.....KKKKKKKKKKKKKKKKRAAA 586

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	764	24.5	462	2	I58179	5HT3 receptor subu
2	764	24.5	489	2	S41757	5-hydroxytryptamin
3	457.5	14.7	464	2	A33523	nicotinic acetylch
4	452	14.5	528	1	ACCH2N	nicotinic acetylch
5	450.5	14.5	466	2	S16333	nicotinic acetylch
6	448.5	14.4	491	1	ACCHNN	nicotinic acetylch
7	446.5	14.3	462	2	S06893	nicotinic acetylch
8	441	14.2	454	2	B39218	nicotinic acetylch
9	441	14.2	503	2	JH0174	nicotinic acetylch
10	440	14.1	502	2	S10505	nicotinic acetylch
11	436.5	14.0	625	2	A26456	nicotinic acetylch
12	435.5	14.0	470	2	A39218	nicotinic acetylch
13	433	13.9	494	2	T09289	nicotinic acetylch
14	432	13.9	423	2	I38056	nicotinic acetylch
15	432	13.9	479	2	A55382	nicotinic acetylch
16	432	13.9	627	2	JC4021	nicotinic acetylch
17	431.5	13.9	499	2	A24572	nicotinic acetylch
18	429.5	13.8	503	2	A53956	nicotinic acetylch
19	429	13.8	455	2	A55972	nicotinic acetylch
20	428.5	13.8	501	2	A25338	nicotinic acetylch
21	427.5	13.7	495	2	S60589	acetylcholine rece
22	427	13.7	501	2	S04607	nicotinic acetylch
23	426.5	13.7	505	2	S07227	nicotinic acetylch
24	426	13.7	512	2	B37014	nicotinic acetylch
25	425	13.6	498	2	G02421	nicotinic acetylch
26	423	13.6	502	1	ACHUA7	nicotinic acetylch
27	423	13.6	622	1	ACCH4N	nicotinic acetylch
28	421	13.5	502	2	JN0113	nicotinic acetylch
29	420.5	13.5	459	2	S14703	nicotinic acetylch
30	420.5	13.5	511	2	A40110	nicotinic acetylch
31	416	13.4	455	2	S51116	nicotinic acetylch
32	416	13.4	560	2	T19622	hypothetical prote
33	415	13.3	502	2	G02259	alpha 7 neuronal n
34	412.5	13.2	501	2	S13873	nicotinic acetylch
35	412.5	13.2	502	2	A37040	nicotinic acetylch
36	410	13.2	502	2	T01378	nicotinic receptor
37	410	13.2	521	2	C28529	nicotinic acetylch
38	409	13.1	452	2	A35721	nicotinic acetylch
39	408	13.1	502	2	A57175	nicotinic acetylch
40	405	13.0	511	2	JH0173	alpha-bungarotoxin
41	405	13.0	517	2	A30992	probable nicotinic
42	402.5	12.9	575	2	S57648	nicotinic acetylch
43	397.5	12.8	521	1	ACFFNN	nicotinic acetylch
44	397	12.7	495	2	B35721	nicotinic acetylch
45	395.5	12.7	517	2	S13875	nicotinic acetylch

ALIGNMENTS

RESULT 1
I58179
5HT3 receptor subunit - rat (fragment)
C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: I58179
R;Isenberg, K.E.; Ukhun, I.A.; Holstad, S.G.; Jafri, S.; Uchida, U.; Zorumski, C.F.; Neuroreport 5, 121-124, 1993
A;Title: Partial cDNA cloning and NGF regulation of a rat 5-HT3 receptor subunit.
A;Reference number: I58179; MUID:94154206
A;Accession: I58179
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-462 <RES>
A;Cross-references: EMBL:U01227; NID:g402245; PIDN:AAA52182.1; PID:g402246
C;Superfamily: acetylcholine receptor

Query Match 24.5%; Score 764; DB 2; Length 462;
Best Local Similarity 37.6%; Pred. No. 1.3e-52;
Matches 170; Conservative 88; Mismatches 142; Indels 52; Gaps 12;

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Qy      64 RKPFRPVTNISVPTQVNISFAMSAILDVNEQLHLLSSFLWLEMVWDNPFISWNPEECEGI 123
           :|  |||  :   ||  |:|   | |||:|:|:  :|::::|   | : |: | ||: : :
Db      30 KKGVRPVRDWRKPTLVSIDVIMYAILNVDEKNQVLTTYIWYRQFWTDEFLQWTPEDFDNV 89

Qy     124 TKMSMAAKNLWLPDIFIIELMDVDKTPKGLTAYVSNEGRIRYKKPMKVDSICNLDIFYFP 183
           ||:|:   ::|:||| | | :|| |:|     || ::| ::  ||::: : |:|||: ||
Db      90 TKLSIPTDSIWVPDILINEFVDVGKSPSIPYVYVHHQGEVQNYKPLQLVTACSLDIYNFP 149

Qy     184 FDQQNCTLTFSSFLYTVDSMLLDMEKEVW---EITDASRNILQTHGEWELLGLSKATAKL 240
           || |||:|||:|:|:|:     |:   :|   |   : ::|    |||||||:     :
Db     150 FDVQNCSLTFTSWLHTIQ----DINISLWRTPEEVRSDKSIFINQGEWELLGVFTKFQEF 205

Qy     241 S-RGGNLYDQIVFYVAIRRRPSLYVINLLVPSGFLVAIDALSFYLPVKSGNRVPFKITLL 299
           |    | | :: ||| ||||  | ::||:|| ||: :| : | ||  || || ||||||
Db     206 SIETSNSYAEMKFYVVIRRRPLFYAVSLLLPSIFLMVVDIVGFCLPPDSGERVSFKITLL 265

Qy     300 LGYNVFLLMMSDLLPTSG--TPLIGVYFALCLSLMVGSLLETIFITHLLHVATTQPPPLP 357
           |||:|||:::|| || :   |||||||| :|::|:| || ||||  |:|    |  |:|
Db     266 LGYSVFLIIVSDTLPATAIRTPLIGVYFVVCMALLVISLAETIFIVQLVHKQDLQ-RPVP 324

Qy     358 RWLHSLLLH------C--NSPGRCCPTAPQKENK-----GPGLTPTHLPGVKEPEVSA-- 402
            ||  |:|       |    |    | |  : ||       |   :|:   :: | ::
Db     325 DWLRHLVLDRIAWLLCLGEQPMAHRPPATFQANKTDDCSAMGNHCSHVGSPQDLEKTSRS 384

Qy     403 --GQMPGPAEAELTGGSEWTRAQREHEAQKQHSVEL----------WLQFSHAMDAMLFR 450
             :| | || |       |   :  :  :||:|           ||:  : :| :|||
Db     385 RDSPLPPPREASLA-----VRGLLQELSSIRHSLEKRDEMREVARDWLRVGYVLDRLLFR 439

Qy     451 LYLLFMASSIITVICLWNTAGAHLPTSVWSFS 482
           :||| : :  ||:: ||         |:| :|
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